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#10

OIPE

## RAW SEQUENCE LISTING

DATE: 08/14/2001

PATENT APPLICATION: US/09/759,281B

TIME: 09:15:52

Input Set : A:\41826cip.app

Output Set: N:\CRF3\08142001\I759281B.raw

ENTERED

3 <110> APPLICANT: PEREGRINO FERREIRA, PAULO CESAR  
 4 KROON, ERNA GEESSIEN  
 5 PIMENTA DOS REIS, JENNER KARLISSEN  
 6 FORTES FERRAZ, ISABELLA BIAS  
 7 CERQUEIRA LEITE, ROMULO  
 9 <120> TITLE OF INVENTION: METHOD AND COMPOSITION FOR THE DIAGNOSIS OF EQUINE  
 10 INFECTIOUS ANEMIA VIRUS DISEASE BY USING THE  
 11 RECOMBINANT CAPSID PROTEIN VIRUS (P26)  
 13 <130> FILE REFERENCE: 41826 CIP  
 15 <140> CURRENT APPLICATION NUMBER: 09/759,281B  
 16 <141> CURRENT FILING DATE: 2001-01-16  
 18 <150> PRIOR APPLICATION NUMBER: 09/331,262  
 19 <151> PRIOR FILING DATE: 1999-07-13  
 21 <150> PRIOR APPLICATION NUMBER: PCT/BR97/00081  
 22 <151> PRIOR FILING DATE: 1997-12-19  
 24 <150> PRIOR APPLICATION NUMBER: PI 9606273-8  
 25 <151> PRIOR FILING DATE: 1996-12-18  
 27 <160> NUMBER OF SEQ ID NOS: 1  
 29 <170> SOFTWARE: PatentIn Ver. 2.1  
 31 <210> SEQ ID NO: 1  
 32 <211> LENGTH: 318  
 33 <212> TYPE: PRT  
 34 <213> ORGANISM: Equine infectious anemia virus  
 36 <400> SEQUENCE: 1  
 37 His His His His His His Gly Ser Pro Gly Asn Pro Leu Thr Trp Ser  
 38 1 5 10 15  
 40 Lys Ala Leu Lys Lys Leu Glu Lys Val Thr Val Gln Gly Ser Gln Lys  
 41 20 25 30  
 43 Leu Thr Thr Gly Asn Cys Asn Trp Ala Leu Ser Leu Val Asp Leu Phe  
 44 35 40 45  
 46 His Asp Thr Asn Phe Val Lys Glu Lys Asp Trp Gln Leu Arg Asp Val  
 47 50 55 60  
 49 Ile Pro Leu Leu Glu Asp Val Thr Gln Thr Val Ser Gly Gln Glu Arg  
 50 65 70 75 80  
 52 Glu Ala Phe Glu Arg Thr Trp Trp Ala Ile Ser Ala Val Lys Met Gly  
 53 85 90 95  
 55 Leu Gln Ile Asn Asn Val Val Asp Gly Lys Ala Ser Phe Gln Leu Leu  
 56 100 105 110  
 58 Arg Ala Lys Tyr Glu Lys Lys Thr Ala Asn Lys Lys Gln Ser Glu Pro  
 59 115 120 125  
 61 Ser Glu Glu Tyr Pro Ile Met Ile Asp Gly Ala Gly Asn Arg Asn Phe  
 62 130 135 140  
 64 Arg Pro Leu Thr Pro Arg Gly Tyr Thr Thr Trp Val Asn Thr Ile Gln  
 65 145 150 155 160  
 67 Thr Asn Gly Leu Leu Asn Glu Ala Ser Gln Asn Leu Phe Gly Ile Leu  
 68 165 170 175  
 70 Ser Val Asp Cys Thr Ser Glu Glu Met Asn Ala Phe Leu Asp Val Val

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```

71          180          185          190
73 Pro Gly Gln Ala Gly Gln Lys Gln Ile Leu Leu Asp Ala Ile Asp Lys
74          195          200          205
76 Ile Ala Asp Asp Trp Asp Asn Arg His Pro Leu Pro Asn Ala Pro Leu
77          210          215          220
79 Val Ala Pro Pro Gln Gly Pro Ile Pro Met Thr Ala Arg Phe Ile Arg
80 225          230          235          240
82 Gly Leu Gly Val Pro Arg Glu Arg Gln Met Glu Pro Asn Cys Val Val
83          245          250          255
85 Gln Ser Phe Gly Val Ile Gly Gln Ala His Leu Glu Leu Pro Arg Pro
86          260          265          270
88 Asn Lys Arg Ile Arg Asn Gln Ser Phe Asn Gln Tyr Asn Cys Ser Ile
89          275          280          285
91 Asn Asn Lys Thr Glu Leu Glu Thr Trp Lys Leu Val Lys Thr Ser Gly
92          290          295          300
94 Val Thr Pro Leu Pro Ile Ser Ser Glu Ala Asn Thr Gly Leu
95 305          310          315

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VERIFICATION SUMMARY

DATE: 08/14/2001

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## Annex 1

### BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

Score = 444 bits (1143), Expect = e-123

Identities = 212/243 (87%), Positives = 229/243 (93%)

| \_\_\_\_\_  
- \_\_\_\_\_

Query: 2 GDPLTWSKALKKLEKVTVQGSQKLTGNCNWALSLVDLFHDTNFKVKEKDWQLRDVIPLLE 61  
G+PLTWSKALKKL+KVTVQGSQKLTGNCNWALSLVDLFHDTNFKV+KDWQLRDVIPLL+  
Sbjct:10 GNPLTWSKALKKLQKVTVQGSQKLTGNCNWALSLVDLFHDTNFKVQKDWQLRDVIPLLQ 69

Query: 62 DVTQTLSGQEREAFERTWWAISAVKMGLQINNVDGKASFQLLRKYEKKTANKKQSEPS 121  
DVTQT+SGQ+R+AF+RTWWAISAVKMGLQINNVDGKASFQLLRKAY+KKTANKKQS+PS  
Sbjct: 70 DVTQTVSGQQRQAFQRTWWAISAVKMGLQINNVDGKASFQLLRKAYQKKTANKKQSQPS 129

Query: 122 EEYPIMIDGAGNRNFRPLTPRGYTTWVNTIQTNGLLNEASQNLFGILSVDCTSEEMNAFL 181  
++YPIMIDGAGNRNFRPLTPRGYTTWVNTIQTNGLLN+ASQNLFGILSVDCTS++MNAFL  
Sbjct: 130 QQYPIMIDGAGNRNFRPLTPRGYTTWVNTIQTNGLLNQASQNLFGILSVDCTSQQMNAFL 189

Query: 182 DVVPGQAGQKQXXXXXXXXXXXXXXXXNRHPLPNAPLVAPPQGPIPMTARFIRGLGVPRERQ 241  
DVVPGQAGQKQ NRHPLPNAPLVAPPQGPIPMTARFIRGLGVPR+RQ  
Sbjct: 190 DVVPGQAGQKQILLDAIDKIADDWDNRHPLPNAPLVAPPQGPIPMTARFIRGLGVPRQRQ 249

Query: 242 MEP 244  
M+P  
Sbjct: 250 MQP 252

Query: ACCESSION M16575 K03334 M11337 M14855

REFERENCE 7 (bases 1 to 8344)

Kawakami,T., Sherman,L., Dahlberg,J., Gazit,A., Yaniv,A., Tronick,S.R.  
and Aaronson,S.A. Nucleotide sequence analysis of equine infectious  
anemia virus proviral DNA. Virology 158 (2), 300-312 (1987)

Sbjct: proposed sequence of instant invention

C

## ANNEX 2

LOCUS EIAVCG 8407 bp ss-RNA linear VRL 11-AUG-1995  
DEFINITION Equine infectious anemia virus proviral DNA, complete genome.  
ACCESSION M16575 K03334 M11337 M14855  
VERSION M16575.1 GI:323836  
KEYWORDS complete genome; env protein; gag protein; glycoprotein; pol protein; polymerase.  
SOURCE Equine infectious anemia virus  
ORGANISM Equine infectious anemia virus Viruses; Retrovird viruses; Retroviridae; Lentivirus; Equine lentiviruses.  
REFERENCE 6 (bases 1 to 8407)  
AUTHORS Kawakami,T., Sherman,L., Dahlberg,J.E., Gazit,A., Yaniv,Y., Tronick,S.R. and Aaronson,S.A. JOURNAL Unpublished (1987)  
REFERENCE 7 (bases 1 to 8344)  
AUTHORS Kawakami,T., Sherman,L., Dahlberg,J., Gazit,A., Yaniv,A., Tronick,S.R. and Aaronson,S.A. Nucleotide sequence analysis of equine infectious anemia virus proviral DNA. Virology 158 (2), 300-312 (1987)  
MEDLINE 87236196 PUBMED 3035786  
COMMENT Original source text: Equine infectious anemia virus (EIAV) proviral DNA, (clones 1369 and 409-2 [1]). [2] sites; peptide coding regions. [6] revises [1]. [8] sites; sequence correction position 5348. Draft entry and computer-readable sequence for [6] kindly provided by S.Tronick, 10-NOV-1987.

FEATURES	Location/Qualifiers
source	1..8407 /organism="Equine infectious anemia virus" /db_xref="taxon:11665"
LTR	1..321 /note="5' LTR"
repeat region	208..>208 /note="R repeat 5' copy"
misc binding	325..342 /bound_moiety="Lys-tRNA primer"
variation	342 /note="c in [7], t in [3]" /replace="t"
CDS	465..1925 /note="465 is the position of the first start codon in the open reading frame/codon_start=1/product="gag protein/protein_id="AAB59861.1/db_xref="GI:323837/translation="

MGDPLTWSKALKKLEKVTVQGSQKLTTGNCNWALSLVDLFHDTN  
FVKEKDWQLRDVIPLEEDVTQTLSGQEREAFERTWWAISAVKMGLQINNVDGKASFQ  
LLRAKYEKKTANKKQSEPSEEYPIMIDGAGNRNFRPLTPRGYTTWNTIQTNGLLNEA  
SQNLFGILSVDDCTSEEMNAFLDVVPGQAGQKQILLDAIDKIADDWDNRHPLPNAPLVA  
PPQGPIPMPTARFIRGLGVPRERQMEPAFDQFRQTYRQWIIIEAMSEGIKVMIGKPKAQN  
IRQGAKEPYPEFVDRLLSQIKSEGHPEISKFLDTLTIQNANEECRNAMRHLRPEDT  
LEEKMYACRDIGTTKQKMMLLAKALQTGLAGPFGKGGALGGPLKAAQTCYNCGKPGHL  
SSQCRAPKVCFKCKQPGHFSKQCRSVPKNGKQGAQGRPQKQTFPIQQKSQHNKSVVQE  
TPQTQNLYPDLSEIKKEYNVKEKDQVEDLNLDLWE"